



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ALBERTSEN, HANS  
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HEDGE, PHILIP J.  
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(ii) TITLE OF INVENTION: APC ANTIBODIES

(iii) NUMBER OF SEQUENCES: [102] 154

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA  
(F) ZIP: 20001-4598

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/442,489  
(B) FILING DATE: 18-NOV-1999  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/452,654  
(B) FILING DATE: 25-MAY-1995

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/289,548  
(B) FILING DATE: 12-AUG-1994

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/741,940  
(B) FILING DATE: 08-AUG-1991

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A.  
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(C) REFERENCE/DOCKET NUMBER: 1107.035574

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9606 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: DP2.5(APC).

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 34..8562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGACTCGGAA ATGAGGTCCA AGGGTAGCCA AGG ATG GCT GCA GCT TCA TAT GAT	54
Met Ala Ala Ala Ser Tyr Asp	
1                       5	
CAG TTG TTA AAG CAA GTT GAG GCA CTG AAG ATG GAG AAC TCA AAT CTT	102
Gln Leu Leu Lys Gln Val Glu Ala Leu Lys Met Glu Asn Ser Asn Leu	
10                      15                      20	
CGA CAA GAG CTA GAA GAT AAT TCC AAT CAT CTT ACA AAA CTG GAA ACT	150
Arg Gln Glu Leu Glu Asp Asn Ser Asn His Leu Thr Lys Leu Glu Thr	
25                      30                      35	
GAG GCA TCT AAT ATG AAG GAA GTA CTT AAA CAA CTA CAA GGA AGT ATT	198
Glu Ala Ser Asn Met Lys Glu Val Leu Lys Gln Leu Gln Gly Ser Ile	

40	45	50	55	
GAA GAT GAA GCT ATG GCT TCT TCT GGA CAG ATT GAT TTA TTA GAG CGT Glu Asp Glu Ala Met Ala Ser Ser Gly Gln Ile Asp Leu Leu Glu Arg	60	65	70	246
CTT AAA GAG CTT AAC TTA GAT AGC AGT AAT TTC CCT GGA GTA AAA CTG Leu Lys Glu Leu Asn Leu Asp Ser Ser Asn Phe Pro Gly Val Lys Leu	75	80	85	294
CGG TCA AAA ATG TCC CTC CGT TCT TAT GGA AGC CGG GAA GGA TCT GTA Arg Ser Lys Met Ser Leu Arg Ser Tyr Gly Ser Arg Glu Gly Ser Val	90	95	100	342
TCA AGC CGT TCT GGA GAG TGC AGT CCT GTT CCT ATG GGT TCA TTT CCA Ser Ser Arg Ser Gly Glu Cys Ser Pro Val Pro Met Gly Ser Phe Pro	105	110	115	390
AGA AGA GGG TTT GTA AAT GGA AGC AGA GAA AGT ACT GGT TAT TTA GAA Arg Arg Gly Phe Val Asn Gly Ser Arg Glu Ser Thr Gly Tyr Leu Glu	120	125	130	438
135				
GAA CTT GAG AAA GAG AGG TCA TTG CTT CTT GCT GAT CTT GAC AAA GAA Glu Leu Glu Lys Glu Arg Ser Leu Leu Leu Ala Asp Leu Asp Lys Glu	140	145	150	486
Glu Lys Glu Lys Asp Trp Tyr Ala Gln Leu Gln Asn Leu Thr Lys	155	160	165	534
AGA ATA GAT AGT CTT CCT TTA ACT GAA AAT TTT TCC TTA CAA ACA GAT Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr Asp	170	175	180	582
TTG ACC AGA AGG CAA TTG GAA TAT GAA GCA AGG CAA ATC AGA GTT GCG Leu Thr Arg Arg Gln Leu Glu Tyr Glu Ala Arg Gln Ile Arg Val Ala	185	190	195	630
ATG GAA GAA CAA CTA GGT ACC TGC CAG GAT ATG GAA AAA CGA GCA CAG Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala Gln	200	205	210	678
215				
CGA AGA ATA GCC AGA ATT CAG CAA ATC GAA AAG GAC ATA CTT CGT ATA Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu Lys Asp Ile Leu Arg Ile	220	225	230	726
CGA CAG CTT TTA CAG TCC CAA GCA ACA GAA GCA GAG AGG TCA TCT CAG Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu Ala Glu Arg Ser Ser Gln	235	240	245	774
AAC AAG CAT GAA ACC GGC TCA CAT GAT GCT GAG CGG CAG AAT GAA GGT				822

Asn Lys His Glu Thr Gly Ser His Asp Ala Glu Arg Gln Asn Glu Gly			
250	255	260	
CAA GGA GTG GGA GAA ATC AAC ATG GCA ACT TCT GGT AAT GGT CAG GGT			870
Gln Gly Val Gly Glu Ile Asn Met Ala Thr Ser Gly Asn Gly Gln Gly			
265	270	275	
TCA ACT ACA CGA ATG GAC CAT GAA ACA GCC AGT GTT TTG AGT TCT AGT			918
Ser Thr Thr Arg Met Asp His Glu Thr Ala Ser Val Leu Ser Ser Ser			
280	285	290	295
AGC ACA CAC TCT GCA CCT CGA AGG CTG ACA AGT CAT CTG GGA ACC AAG			966
Ser Thr His Ser Ala Pro Arg Arg Leu Thr Ser His Leu Gly Thr Lys			
300	305	310	
GTG GAA ATG GTG TAT TCA TTG TCA ATG CTT GGT ACT CAT GAT AAG			1014
Val Glu Met Val Tyr Ser Leu Leu Ser Met Leu Gly Thr His Asp Lys			
315	320	325	
GAT GAT ATG TCG CGA ACT TTG CTA GCT ATG TCT AGC TCC CAA GAC AGC			1062
Asp Asp Met Ser Arg Thr Leu Leu Ala Met Ser Ser Ser Gln Asp Ser			
330	335	340	
TGT ATA TCC ATG CGA CAG TCT GGA TGT CTT CCT CTC CTC ATC CAG CTT			1110
Cys Ile Ser Met Arg Gln Ser Gly Cys Leu Pro Leu Leu Ile Gln Leu			
345	350	355	
TTA CAT GGC AAT GAC AAA GAC TCT GTA TTG TTG GGA AAT TCC CGG GGC			1158
Leu His Gly Asn Asp Lys Asp Ser Val Leu Leu Gly Asn Ser Arg Gly			
360	365	370	375
AGT AAA GAG GCT CGG GCC AGG GCC AGT GCA GCA CTC CAC AAC ATC ATT			1206
Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala Ala Leu His Asn Ile Ile			
380	385	390	
CAC TCA CAG CCT GAT GAC AAG AGA GGC AGG CGT GAA ATC CGA GTC CTT			1254
His Ser Gln Pro Asp Asp Lys Arg Gly Arg Arg Glu Ile Arg Val Leu			
395	400	405	
CAT CTT TTG GAA CAG ATA CGC GCT TAC TGT GAA ACC TGT TGG GAG TGG			1302
His Leu Leu Glu Gln Ile Arg Ala Tyr Cys Glu Thr Cys Trp Glu Trp			
410	415	420	
CAG GAA GCT CAT GAA CCA GGC ATG GAC CAG GAC AAA AAT CCA ATG CCA			1350
Gln Glu Ala His Glu Pro Gly Met Asp Gln Asp Lys Asn Pro Met Pro			
425	430	435	
GCT CCT GTT GAA CAT CAG ATC TGT CCT GCT GTG TGT GTT CTA ATG AAA			1398
Ala Pro Val Glu His Gln Ile Cys Pro Ala Val Cys Val Leu Met Lys			
440	445	450	455

CTT TCA TTT GAT GAA GAG CAT AGA CAT GCA ATG AAT GAA CTA GGG GGA Leu Ser Phe Asp Glu Glu His Arg His Ala Met Asn Glu Leu Gly Gly 460 465 470	1446
CTA CAG GCC ATT GCA GAA TTA TTG CAA GTG GAC TGT GAA ATG TAT GGG Leu Gln Ala Ile Ala Glu Leu Leu Gln Val Asp Cys Glu Met Tyr Gly 475 480 485	1494
CTT ACT AAT GAC CAC TAC AGT ATT ACA CTA AGA CGA TAT GCT GGA ATG Leu Thr Asn Asp His Tyr Ser Ile Thr Leu Arg Arg Tyr Ala Gly Met 490 495 500	1542
GCT TTG ACA AAC TTG ACT TTT GGA GAT GTA GCC AAC AAG GCT ACG CTA Ala Leu Thr Asn Leu Thr Phe Gly Asp Val Ala Asn Lys Ala Thr Leu 505 510 515	1590
TGC TCT ATG AAA GGC TGC ATG AGA GCA CTT GTG GCC CAA CTA AAA TCT Cys Ser Met Lys Gly Cys Met Arg Ala Leu Val Ala Gln Leu Lys Ser 520 525 530 535	1638
GAA AGT GAA GAC TTA CAG CAG GTT ATT GCA AGT GTT TTG AGG AAT TTG Glu Ser Glu Asp Leu Gln Gln Val Ile Ala Ser Val Leu Arg Asn Leu 540 545 550	1686
TCT TGG CGA GCA GAT GTA AAT AGT AAA AAG ACG TTG CGA GAA GTT GGA Ser Trp Arg Ala Asp Val Asn Ser Lys Lys Thr Leu Arg Glu Val Gly 555 560 565	1734
AGT GTG AAA GCA TTG ATG GAA TGT GCT TTA GAA GTT AAA AAG GAA TCA Ser Val Lys Ala Leu Met Glu Cys Ala Leu Glu Val Lys Lys Glu Ser 570 575 580	1782
ACC CTC AAA AGC GTA TTG AGT GCC TTA TGG AAT TTG TCA GCA CAT TGC Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn Leu Ser Ala His Cys 585 590 595	1830
ACT GAG AAT AAA GCT GAT ATA TGT GCT GTA GAT GGT GCA CTT GCA TTT Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asp Gly Ala Leu Ala Phe 600 605 610 615	1878
TTG GTT GGC ACT CTT ACT TAC CGG AGC CAG ACA AAC ACT TTA GCC ATT Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln Thr Asn Thr Leu Ala Ile 620 625 630	1926
ATT GAA AGT GGA GGT GGG ATA TTA CGG AAT GTG TCC AGC TTG ATA GCT Ile Glu Ser Gly Gly Ile Leu Arg Asn Val Ser Ser Leu Ile Ala 635 640 645	1974
ACA AAT GAG GAC CAC AGG CAA ATC CTA AGA GAG AAC AAC TGT CTA CAA Thr Asn Glu Asp His Arg Gln Ile Leu Arg Glu Asn Asn Cys Leu Gln 650 655 660	2022

ACT TTA TTA CAA CAC TTA AAA TCT CAT AGT TTG ACA ATA GTC AGT AAT Thr Leu Leu Gln His Leu Lys Ser His Ser Leu Thr Ile Val Ser Asn 665 670 675	2070
GCA TGT GGA ACT TTG TGG AAT CTC TCA GCA AGA AAT CCT AAA GAC CAG Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg Asn Pro Lys Asp Gln 680 685 690 695	2118
GAA GCA TTA TGG GAC ATG GGG GCA GTT AGC ATG CTC AAG AAC CTC ATT Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met Leu Lys Asn Leu Ile 700 705 710	2166
CAT TCA AAG CAC AAA ATG ATT GCT ATG GGA AGT GCT GCA GCT TTA AGG His Ser Lys His Lys Met Ile Ala Met Gly Ser Ala Ala Ala Leu Arg 715 720 725	2214
AAT CTC ATG GCA AAT AGG CCT GCG AAG TAC AAG GAT GCC AAT ATT ATG Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr Lys Asp Ala Asn Ile Met 730 735 740	2262
TCT CCT GGC TCA AGC TTG CCA TCT CTT CAT GTT AGG AAA CAA AAA GCC Ser Pro Gly Ser Ser Leu Pro Ser Leu His Val Arg Lys Gln Lys Ala 745 750 755	2310
CTA GAA GCA GAA TTA GAT GCT CAG CAC TTA TCA GAA ACT TTT GAC AAT Leu Glu Ala Glu Leu Asp Ala Gln His Leu Ser Glu Thr Phe Asp Asn 760 765 770 775	2358
ATA GAC AAT TTA AGT CCC AAG GCA TCT CAT CGT AGT AAG CAG AGA CAC Ile Asp Asn Leu Ser Pro Lys Ala Ser His Arg Ser Lys Gln Arg His 780 785 790	2406
AAG CAA AGT CTC TAT GGT GAT TAT GTT TTT GAC ACC AAT CGA CAT GAT Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe Asp Thr Asn Arg His Asp 795 800 805	2454
GAT AAT AGG TCA GAC AAT TTT AAT ACT GGC AAC ATG ACT GTC CTT TCA Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly Asn Met Thr Val Leu Ser 810 815 820	2502
CCA TAT TTG AAT ACT ACA GTG TTA CCC AGC TCC TCT TCA TCA AGA GGA Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser Ser Ser Arg Gly 825 830 835	2550
AGC TTA GAT AGT TCT CGT TCT GAA AAA GAT AGA AGT TTG GAG AGA GAA Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp Arg Ser Leu Glu Arg Glu 840 845 850 855	2598
CGC GGA ATT GGT CTA GGC AAC TAC CAT CCA GCA ACA GAA AAT CCA GGA Arg Gly Ile Gly Leu Gly Asn Tyr His Pro Ala Thr Glu Asn Pro Gly	2646

	860	865	870	
ACT TCT TCA AAG CGA GGT TTG CAG ATC TCC ACC ACT GCA GCC CAG ATT Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser Thr Thr Ala Ala Gln Ile	875	880	885	2694
GCC AAA GTC ATG GAA GAA GTG TCA GCC ATT CAT ACC TCT CAG GAA GAC Ala Lys Val Met Glu Glu Val Ser Ala Ile His Thr Ser Gln Glu Asp	890	895	900	2742
AGA AGT TCT GGG TCT ACC ACT GAA TTA CAT TGT GTG ACA GAT GAG AGA Arg Ser Ser Gly Ser Thr Thr Glu Leu His Cys Val Thr Asp Glu Arg	905	910	915	2790
AAT GCA CTT AGA AGA AGC TCT GCT GCC CAT ACA CAT TCA AAC ACT TAC Asn Ala Leu Arg Arg Ser Ser Ala Ala His Thr His Ser Asn Thr Tyr	920	925	930	2838
AAT TTC ACT AAG TCG GAA AAT TCA AAT AGG ACA TGT TCT ATG CCT TAT Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg Thr Cys Ser Met Pro Tyr	940	945	950	2886
GCC AAA TTA GAA TAC AAG AGA TCT TCA AAT GAT AGT TTA AAT AGT GTC Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn Asp Ser Leu Asn Ser Val	955	960	965	2934
AGT AGT AAT GAT GGT TAT GGT AAA AGA GGT CAA ATG AAA CCC TCG ATT Ser Ser Asn Asp Gly Tyr Gly Lys Arg Gly Gln Met Lys Pro Ser Ile	970	975	980	2982
GAA TCC TAT TCT GAA GAT GAT GAA AGT AAG TTT TGC AGT TAT GGT CAA Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys Phe Cys Ser Tyr Gly Gln	985	990	995	3030
TAC CCA GCC GAC CTA GCC CAT AAA ATA CAT AGT GCA AAT CAT ATG GAT Tyr Pro Ala Asp Leu Ala His Lys Ile His Ser Ala Asn His Met Asp	1000	1005	1010	3078
GAT AAT GAT GGA GAA CTA GAT ACA CCA ATA AAT TAT AGT CTT AAA TAT Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile Asn Tyr Ser Leu Lys Tyr	1020	1025	1030	3126
TCA GAT GAG CAG TTG AAC TCT GGA AGG CAA AGT CCT TCA CAG AAT GAA Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln Ser Pro Ser Gln Asn Glu	1035	1040	1045	3174
AGA TGG GCA AGA CCC AAA CAC ATA ATA GAA GAT GAA ATA AAA CAA AGT Arg Trp Ala Arg Pro Lys His Ile Ile Glu Asp Glu Ile Lys Gln Ser	1050	1055	1060	3222
GAG CAA AGA CAA TCA AGG AAT CAA AGT ACA ACT TAT CCT GTT TAT ACT				3270

Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr Thr Tyr Pro Val Tyr Thr			
1065	1070	1075	
GAG AGC ACT GAT GAT AAA CAC CTC AAG TTC CAA CCA CAT TTT GGA CAG			3318
Glu Ser Thr Asp Asp Lys His Leu Lys Phe Gln Pro His Phe Gly Gln			
1080	1085	1090	1095
CAG GAA TGT GTT TCT CCA TAC AGG TCA CGG GGA GCC AAT GGT TCA GAA			3366
Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg Gly Ala Asn Gly Ser Glu			
1100	1105	1110	
ACA AAT CGA GTG GGT TCT AAT CAT GGA ATT AAT CAA AAT GTA AGC CAG			3414
Thr Asn Arg Val Gly Ser Asn His Gly Ile Asn Gln Asn Val Ser Gln			
1115	1120	1125	
TCT TTG TGT CAA GAA GAT GAC TAT GAA GAT GAT AAG CCT ACC AAT TAT			3462
Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp Asp Lys Pro Thr Asn Tyr			
1130	1135	1140	
AGT GAA CGT TAC TCT GAA GAA CAG CAT GAA GAA GAG AGA CCA			3510
Ser Glu Arg Tyr Ser Glu Glu Glu Gln His Glu Glu Glu Arg Pro			
1145	1150	1155	
ACA AAT TAT AGC ATA AAA TAT AAT GAA GAG AAA CGT CAT GTG GAT CAG			3558
Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu Lys Arg His Val Asp Gln			
1160	1165	1170	1175
CCT ATT GAT TAT AGT TTA AAA TAT GCC ACA GAT ATT CCT TCA TCA CAG			3606
Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr Asp Ile Pro Ser Ser Gln			
1180	1185	1190	
AAA CAG TCA TTT TCA TTC TCA AAG AGT TCA TCT GGA CAA AGC AGT AAA			3654
Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser Gly Gln Ser Ser Lys			
1195	1200	1205	
ACC GAA CAT ATG TCT TCA AGC AGT GAG AAT ACG TCC ACA CCT TCA TCT			3702
Thr Glu His Met Ser Ser Ser Glu Asn Thr Ser Thr Pro Ser Ser			
1210	1215	1220	
AAT GCC AAG AGG CAG AAT CAG CTC CAT CCA AGT TCT GCA CAG AGT AGA			3750
Asn Ala Lys Arg Gln Asn Gln Leu His Pro Ser Ser Ala Gln Ser Arg			
1225	1230	1235	
AGT GGT CAG CCT CAA AAG GCT GCC ACT TGC AAA GTT TCT TCT ATT AAC			3798
Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys Lys Val Ser Ser Ile Asn			
1240	1245	1250	1255
CAA GAA ACA ATA CAG ACT TAT TGT GTA GAA GAT ACT CCA ATA TGT TTT			3846
Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe			
1260	1265	1270	

TCA AGA TGT AGT TCA TTA TCA TCT TTG TCA TCA GCT GAA GAT GAA ATA Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser Ser Ala Glu Asp Glu Ile 1275 1280 1285	3894
GGA TGT AAT CAG ACG ACA CAG GAA GCA GAT TCT GCT AAT ACC CTG CAA Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp Ser Ala Asn Thr Leu Gln 1290 1295 1300	3942
ATA GCA GAA ATA AAA GGA AAG ATT GGA ACT AGG TCA GCT GAA GAT CCT Ile Ala Glu Ile Lys Gly Lys Ile Gly Thr Arg Ser Ala Glu Asp Pro 1305 1310 1315	3990
GTG AGC GAA GTT CCA GCA GTG TCA CAG CAC CCT AGA ACC AAA TCC AGC Val Ser Glu Val Pro Ala Val Ser Gln His Pro Arg Thr Lys Ser Ser 1320 1325 1330 1335	4038
AGA CTG CAG GGT TCT AGT TTA TCT TCA GAA TCA GCC AGG CAC AAA GCT Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu Ser Ala Arg His Lys Ala 1340 1345 1350	4086
GTT GAA TTT CCT TCA GGA GCG AAA TCT CCC TCC AAA AGT GGT GCT CAG Val Glu Phe Pro Ser Gly Ala Lys Ser Pro Ser Lys Ser Gly Ala Gln 1355 1360 1365	4134
ACA CCC AAA AGT CCA CCT GAA CAC TAT GTT CAG GAG ACC CCA CTC ATG Thr Pro Lys Ser Pro Pro Glu His Tyr Val Gln Glu Thr Pro Leu Met 1370 1375 1380	4182
TTT AGC AGA TGT ACT TCT GTC AGT TCA CTT GAT AGT TTT GAG AGT CGT Phe Ser Arg Cys Thr Ser Val Ser Ser Leu Asp Ser Phe Glu Ser Arg 1385 1390 1395	4230
TCG ATT GCC AGC TCC GTT CAG AGT GAA CCA TGC AGT GGA ATG GTA AGT Ser Ile Ala Ser Ser Val Gln Ser Glu Pro Cys Ser Gly Met Val Ser 1400 1405 1410 1415	4278
GGC ATT ATA AGC CCC AGT GAT CTT CCA GAT AGC CCT GGA CAA ACC ATG Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp Ser Pro Gly Gln Thr Met 1420 1425 1430	4326
CCA CCA AGC AGA AGT AAA ACA CCT CCA CCA CCT CCT CAA ACA GCT CAA Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro Pro Gln Thr Ala Gln 1435 1440 1445	4374
ACC AAG CGA GAA GTA CCT AAA AAT AAA GCA CCT ACT GCT GAA AAG AGA Thr Lys Arg Glu Val Pro Lys Asn Lys Ala Pro Thr Ala Glu Lys Arg 1450 1455 1460	4422
GAG AGT GGA CCT AAG CAA GCT GCA GTA AAT GCT GCA GTT CAG AGG GTC Glu Ser Gly Pro Lys Gln Ala Ala Val Asn Ala Val Gln Arg Val 1465 1470 1475	4470

CAG GTT CTT CCA GAT GCT GAT ACT TTA TTA CAT TTT GCC ACA GAA AGT Gln Val Leu Pro Asp Ala Asp Thr Leu Leu His Phe Ala Thr Glu Ser 1480                    1485                    1490                    1495	4518
ACT CCA GAT GGA TTT TCT TGT TCA TCC AGC CTG AGT GCT CTG AGC CTC Thr Pro Asp Gly Phe Ser Cys Ser Ser Leu Ser Ala Leu Ser Leu 1500                    1505                    1510	4566
GAT GAG CCA TTT ATA CAG AAA GAT GTG GAA TTA AGA ATA ATG CCT CCA Asp Glu Pro Phe Ile Gln Lys Asp Val Glu Leu Arg Ile Met Pro Pro 1515                    1520                    1525	4614
GTT CAG GAA AAT GAC AAT GGG AAT GAA ACA GAA TCA GAG CAG CCT AAA Val Gln Glu Asn Asp Asn Gly Asn Glu Thr Glu Ser Glu Gln Pro Lys 1530                    1535                    1540	4662
GAA TCA AAT GAA AAC CAA GAG AAA GAG GCA GAA AAA ACT ATT GAT TCT Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala Glu Lys Thr Ile Asp Ser 1545                    1550                    1555	4710
GAA AAG GAC CTA TTA GAT GAT TCA GAT GAT GAT ATT GAA ATA CTA Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp Asp Ile Glu Ile Leu 1560                    1565                    1570                    1575	4758
GAA GAA TGT ATT ATT TCT GCC ATG CCA ACA AAG TCA TCA CGT AAA GGC Glu Glu Cys Ile Ile Ser Ala Met Pro Thr Lys Ser Ser Arg Lys Gly 1580                    1585                    1590	4806
AAA AAG CCA GCC CAG ACT GCT TCA AAA TTA CCT CCA CCT GTG GCA AGG Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu Pro Pro Pro Val Ala Arg 1595                    1600                    1605	4854
AAA CCA AGT CAG CTG CCT GTG TAC AAA CTT CTA CCA TCA CAA AAC AGG Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu Leu Pro Ser Gln Asn Arg 1610                    1615                    1620	4902
TTG CAA CCC CAA AAG CAT GTT AGT TTT ACA CCG GGG GAT GAT ATG CCA Leu Gln Pro Gln Lys His Val Ser Phe Thr Pro Gly Asp Asp Met Pro 1625                    1630                    1635	4950
CGG GTG TAT TGT GTT GAA GGG ACA CCT ATA AAC TTT TCC ACA GCT ACA Arg Val Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr 1640                    1645                    1650                    1655	4998
TCT CTA AGT GAT CTA ACA ATC GAA TCC CCT CCA AAT GAG TTA GCT GCT Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro Pro Asn Glu Leu Ala Ala 1660                    1665                    1670	5046
GGA GAA GGA GTT AGA GGA GGA GCA CAG TCA GGT GAA TTT GAA AAA CGA Gly Glu Gly Val Arg Gly Gly Ala Gln Ser Gly Glu Phe Glu Lys Arg	5094

1675	1680	1685	
GAT ACC ATT CCT ACA GAA GGC AGA AGT ACA GAT GAG GCT CAA GGA GGA Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr Asp Glu Ala Gln Gly Gly 1690	1695	1700	5142
AAA ACC TCA TCT GTA ACC ATA CCT GAA TTG GAT GAC AAT AAA GCA GAG Lys Thr Ser Ser Val Thr Ile Pro Glu Leu Asp Asp Asn Lys Ala Glu 1705	1710	1715	5190
GAA GGT GAT ATT CTT GCA GAA TGC ATT AAT TCT GCT ATG CCC AAA GGG Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn Ser Ala Met Pro Lys Gly 1720	1725	1730	5238
AAA AGT CAC AAG CCT TTC CGT GTG AAA AAG ATA ATG GAC CAG GTC CAG Lys Ser His Lys Pro Phe Arg Val Lys Lys Ile Met Asp Gln Val Gln 1740	1745	1750	5286
CAA GCA TCT GCG TCG TCT TCT GCA CCC AAC AAA AAT CAG TTA GAT GGT Gln Ala Ser Ala Ser Ser Ala Pro Asn Lys Asn Gln Leu Asp Gly 1755	1760	1765	5334
AAG AAA AAG AAA CCA ACT TCA CCA GTA AAA CCT ATA CCA CAA AAT ACT Lys Lys Lys Pro Thr Ser Pro Val Lys Pro Ile Pro Gln Asn Thr 1770	1775	1780	5382
GAA TAT AGG ACA CGT GTA AGA AAA AAT GCA GAC TCA AAA AAT AAT TTA Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala Asp Ser Lys Asn Asn Leu 1785	1790	1795	5430
AAT GCT GAG AGA GTT TTC TCA GAC AAC AAA GAT TCA AAG AAA CAG AAT Asn Ala Glu Arg Val Phe Ser Asp Asn Lys Asp Ser Lys Lys Gln Asn 1800	1805	1810	5478
TTG AAA AAT AAT TCC AAG GAC TTC AAT GAT AAG CTC CCA AAT AAT GAA Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp Lys Leu Pro Asn Asn Glu 1820	1825	1830	5526
GAT AGA GTC AGA GGA AGT TTT GCT TTT GAT TCA CCT CAT CAT TAC ACG Asp Arg Val Arg Gly Ser Phe Ala Phe Asp Ser Pro His His Tyr Thr 1835	1840	1845	5574
CCT ATT GAA GGA ACT CCT TAC TGT TTT TCA CGA AAT GAT TCT TTG AGT Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu Ser 1850	1855	1860	5622
TCT CTA GAT TTT GAT GAT GAT GTT GAC CTT TCC AGG GAA AAG GCT Ser Leu Asp Phe Asp Asp Asp Val Asp Leu Ser Arg Glu Lys Ala 1865	1870	1875	5670
GAA TTA AGA AAG GCA AAA GAA AAT AAG GAA TCA GAG GCT AAA GTT ACC			5718

Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys	Glu	Ser	Glu	Ala	Lys	Val	Thr	
1880				1885					1890					1895		
AGC	CAC	ACA	GAA	CTA	ACC	TCC	AAC	CAA	CAA	TCA	GCT	AAT	AAG	ACA	CAA	5766
Ser	His	Thr	Glu	Leu	Thr	Ser	Asn	Gln	Gln	Ser	Ala	Asn	Lys	Thr	Gln	
				1900					1905					1910		
GCT	ATT	GCA	AAG	CAG	CCA	ATA	AAT	CGA	GGT	CAG	CCT	AAA	CCC	ATA	CTT	5814
Ala	Ile	Ala	Lys	Gln	Pro	Ile	Asn	Arg	Gly	Gln	Pro	Lys	Pro	Ile	Leu	
				1915					1920					1925		
CAG	AAA	CAA	TCC	ACT	TTT	CCC	CAG	TCA	TCC	AAA	GAC	ATA	CCA	GAC	AGA	5862
Gln	Lys	Gln	Ser	Thr	Phe	Pro	Gln	Ser	Ser	Lys	Asp	Ile	Pro	Asp	Arg	
				1930					1935					1940		
GGG	GCA	GCA	ACT	GAT	GAA	AAG	TTA	CAG	AAT	TTT	GCT	ATT	GAA	AAT	ACT	5910
Gly	Ala	Ala	Thr	Asp	Glu	Lys	Leu	Gln	Asn	Phe	Ala	Ile	Glu	Asn	Thr	
				1945					1950					1955		
CCA	GTT	TGC	TTT	TCT	CAT	AAT	TCC	TCT	CTG	AGT	TCT	CTC	AGT	GAC	ATT	5958
Pro	Val	Cys	Phe	Ser	His	Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Asp	Ile	
				1960					1965					1970		
GAC	CAA	GAA	AAC	AAC	AAT	AAA	GAA	AAT	GAA	CCT	ATC	AAA	GAG	ACT	GAG	6006
Asp	Gln	Glu	Asn	Asn	Asn	Lys	Glu	Asn	Glu	Pro	Ile	Lys	Glu	Thr	Glu	
				1980					1985					1990		
CCC	CCT	GAC	TCA	CAG	GGA	GAA	CCA	AGT	AAA	CCT	CAA	GCA	TCA	GGC	TAT	6054
Pro	Pro	Asp	Ser	Gln	Gly	Glu	Pro	Ser	Lys	Pro	Gln	Ala	Ser	Gly	Tyr	
				1995					2000					2005		
GCT	CCT	AAA	TCA	TTT	CAT	GTT	GAA	GAT	ACC	CCA	GTT	TGT	TTC	TCA	AGA	6102
Ala	Pro	Lys	Ser	Phe	His	Val	Glu	Asp	Thr	Pro	Val	Cys	Phe	Ser	Arg	
				2010					2015					2020		
AAC	AGT	TCT	CTC	AGT	TCT	CTT	AGT	ATT	GAC	TCT	GAA	GAT	GAC	CTG	TTG	6150
Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ile	Asp	Ser	Glu	Asp	Asp	Leu	Leu	
				2025					2030					2035		
CAG	GAA	TGT	ATA	AGC	TCC	GCA	ATG	CCA	AAA	AAG	AAA	AAG	CCT	TCA	AGA	6198
Gln	Glu	Cys	Ile	Ser	Ser	Ala	Met	Pro	Lys	Lys	Lys	Lys	Pro	Ser	Arg	
				2040					2045					2050		
CTC	AAG	GGT	GAT	AAT	GAA	AAA	CAT	AGT	CCC	AGA	AAT	ATG	GGT	GGC	ATA	6246
Leu	Lys	Gly	Asp	Asn	Glu	Lys	His	Ser	Pro	Arg	Asn	Met	Gly	Gly	Ile	
				2060					2065					2070		
TTA	GGT	GAA	GAT	CTG	ACA	CTT	GAT	TTG	AAA	GAT	ATA	CAG	AGA	CCA	GAT	6294
Leu	Gly	Glu	Asp	Leu	Thr	Leu	Asp	Leu	Lys	Asp	Ile	Gln	Arg	Pro	Asp	
				2075					2080					2085		

TCA GAA CAT GGT CTA TCC CCT GAT TCA GAA AAT TTT GAT TGG AAA GCT Ser Glu His Gly Leu Ser Pro Asp Ser Glu Asn Phe Asp Trp Lys Ala 2090 2095 2100	6342
ATT CAG GAA GGT GCA AAT TCC ATA GTA AGT AGT TTA CAT CAA GCT GCT Ile Gln Glu Gly Ala Asn Ser Ile Val Ser Ser Leu His Gln Ala Ala 2105 2110 2115	6390
GCT GCT GCA TGT TTA TCT AGA CAA GCT TCG TCT GAT TCA GAT TCC ATC Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser Ser Asp Ser Asp Ser Ile 2120 2125 2130 2135	6438
CTT TCC CTG AAA TCA GGA ATC TCT CTG GGA TCA CCA TTT CAT CTT ACA Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly Ser Pro Phe His Leu Thr 2140 2145 2150	6486
CCT GAT CAA GAA GAA AAA CCC TTT ACA AGT AAT AAA GGC CCA CGA ATT Pro Asp Gln Glu Lys Pro Phe Thr Ser Asn Lys Gly Pro Arg Ile 2155 2160 2165	6534
CTA AAA CCA GGG GAG AAA AGT ACA TTG GAA ACT AAA AAG ATA GAA TCT Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu Thr Lys Lys Ile Glu Ser 2170 2175 2180	6582
GAA AGT AAA GGA ATC AAA GGA GGA AAA AAA GTT TAT AAA AGT TTG ATT Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys Val Tyr Lys Ser Leu Ile 2185 2190 2195	6630
ACT GGA AAA GTT CGA TCT AAT TCA GAA ATT TCA GGC CAA ATG AAA CAG Thr Gly Lys Val Arg Ser Asn Ser Glu Ile Ser Gly Gln Met Lys Gln 2200 2205 2210 2215	6678
CCC CTT CAA GCA AAC ATG CCT TCA ATC TCT CGA GGC AGG ACA ATG ATT Pro Leu Gln Ala Asn Met Pro Ser Ile Ser Arg Gly Arg Thr Met Ile 2220 2225 2230	6726
CAT ATT CCA GGA GTT CGA AAT AGC TCC TCA AGT ACA AGT CCT GTT TCT His Ile Pro Gly Val Arg Asn Ser Ser Ser Thr Ser Pro Val Ser 2235 2240 2245	6774
AAA AAA GGC CCA CCC CTT AAG ACT CCA GCC TCC AAA AGC CCT AGT GAA Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala Ser Lys Ser Pro Ser Glu 2250 2255 2260	6822
GGT CAA ACA GCC ACC ACT TCT CCT AGA GGA GCC AAG CCA TCT GTG AAA Gly Gln Thr Ala Thr Ser Pro Arg Gly Ala Lys Pro Ser Val Lys 2265 2270 2275	6870
TCA GAA TTA AGC CCT GTT GCC AGG CAG ACA TCC CAA ATA GGT GGG TCA Ser Glu Leu Ser Pro Val Ala Arg Gln Thr Ser Gln Ile Gly Gly Ser 2280 2285 2290 2295	6918

AGT AAA GCA CCT TCT AGA TCA GGA TCT AGA GAT TCG ACC CCT TCA AGA Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg Asp Ser Thr Pro Ser Arg 2300 2305 2310	6966
CCT GCC CAG CAA CCA TTA AGT AGA CCT ATA CAG TCT CCT GGC CGA AAC Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile Gln Ser Pro Gly Arg Asn 2315 2320 2325	7014
TCA ATT TCC CCT GGT AGA AAT GGA ATA AGT CCT CCT AAC AAA TTA TCT Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser Pro Pro Asn Lys Leu Ser 2330 2335 2340	7062
CAA CTT CCA AGG ACA TCA TCC CCT AGT ACT GCT TCA ACT AAG TCC TCA Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr Ala Ser Thr Lys Ser Ser 2345 2350 2355	7110
GGT TCT GGA AAA ATG TCA TAT ACA TCT CCA GGT AGA CAG ATG AGC CAA Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro Gly Arg Gln Met Ser Gln 2360 2365 2370 2375	7158
CAG AAC CTT ACC AAA CAA ACA GGT TTA TCC AAG AAT GCC AGT AGT ATT Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser Lys Asn Ala Ser Ser Ile 2380 2385 2390	7206
CCA AGA AGT GAG TCT GCC TCC AAA GGA CTA AAT CAG ATG AAT AAT GGT Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu Asn Gln Met Asn Asn Gly 2395 2400 2405	7254
AAT GGA GCC AAT AAA AAG GTA GAA CTT TCT AGA ATG TCT TCA ACT AAA Asn Gly Ala Asn Lys Lys Val Glu Leu Ser Arg Met Ser Ser Thr Lys 2410 2415 2420	7302
TCA AGT GGA AGT GAA TCT GAT AGA TCA GAA AGA CCT GTA TTA GTA CGC Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu Arg Pro Val Leu Val Arg 2425 2430 2435	7350
CAG TCA ACT TTC ATC AAA GAA GCT CCA AGC CCA ACC TTA AGA AGA AAA Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser Pro Thr Leu Arg Arg Lys 2440 2445 2450 2455	7398
TTG GAG GAA TCT GCT TCA TTT GAA TCT CTT TCT CCA TCA TCT AGA CCA Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu Ser Pro Ser Ser Arg Pro 2460 2465 2470	7446
GCT TCT CCC ACT AGG TCC CAG GCA CAA ACT CCA GTT TTA AGT CCT TCC Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr Pro Val Leu Ser Pro Ser 2475 2480 2485	7494
CTT CCT GAT ATG TCT CTA TCC ACA CAT TCG TCT GTT CAG GCT GGT GGA Leu Pro Asp Met Ser Leu Ser Thr His Ser Ser Val Gln Ala Gly Gly	7542

2490	2495	2500	
TGG CGA AAA CTC CCA CCT AAT CTC AGT CCC ACT ATA GAG TAT AAT GAT Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro Thr Ile Glu Tyr Asn Asp 2505	2510	2515	7590
GGA AGA CCA GCA AAG CGC CAT GAT ATT GCA CGG TCT CAT TCT GAA AGT Gly Arg Pro Ala Lys Arg His Asp Ile Ala Arg Ser His Ser Glu Ser 2520	2525	2530	7638
CCT TCT AGA CTT CCA ATC AAT AGG TCA GGA ACC TGG AAA CGT GAG CAC Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly Thr Trp Lys Arg Glu His 2540	2545	2550	7686
AGC AAA CAT TCA TCA TCC CTT CCT CGA GTA AGC ACT TGG AGA AGA ACT Ser Lys His Ser Ser Ser Leu Pro Arg Val Ser Thr Trp Arg Arg Thr 2555	2560	2565	7734
GGA AGT TCA TCT TCA ATT CTT TCT GCT TCA TCA GAA TCC AGT GAA AAA Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser Ser Glu Ser Ser Glu Lys 2570	2575	2580	7782
GCA AAA AGT GAG GAT GAA AAA CAT GTG AAC TCT ATT TCA GGA ACC AAA Ala Lys Ser Glu Asp Glu Lys His Val Asn Ser Ile Ser Gly Thr Lys 2585	2590	2595	7830
CAA AGT AAA GAA AAC CAA GTA TCC GCA AAA GGA ACA TGG AGA AAA ATA Gln Ser Lys Glu Asn Gln Val Ser Ala Lys Gly Thr Trp Arg Lys Ile 2600	2605	2610	7878
AAA GAA AAT GAA TTT TCT CCC ACA AAT AGT ACT TCT CAG ACC GTT TCC Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser Thr Ser Gln Thr Val Ser 2620	2625	2630	7926
TCA GGT GCT ACA AAT GGT GCT GAA TCA AAG ACT CTA ATT TAT CAA ATG Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys Thr Leu Ile Tyr Gln Met 2635	2640	2645	7974
GCA CCT GCT GTT TCT AAA ACA GAG GAT GTT TGG GTG AGA ATT GAG GAC Ala Pro Ala Val Ser Lys Thr Glu Asp Val Trp Val Arg Ile Glu Asp 2650	2655	2660	8022
TGT CCC ATT AAC AAT CCT AGA TCT GGA AGA TCT CCC ACA GGT AAT ACT Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg Ser Pro Thr Gly Asn Thr 2665	2670	2675	8070
CCC CCG GTG ATT GAC AGT GTT TCA GAA AAG GCA AAT CCA AAC ATT AAA Pro Pro Val Ile Asp Ser Val Ser Glu Lys Ala Asn Pro Asn Ile Lys 2680	2685	2690	8118
GAT TCA AAA GAT AAT CAG GCA AAA CAA AAT GTG GGT AAT GGC AGT GTT			8166

Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn Val Gly Asn Gly Ser Val			
2700	2705	2710	
CCC ATG CGT ACC GTG GGT TTG GAA AAT CGC CTG ACC TCC TTT ATT CAG			8214
Pro Met Arg Thr Val Gly Leu Glu Asn Arg Leu Thr Ser Phe Ile Gln			
2715	2720	2725	
GTG GAT GCC CCT GAC CAA AAA GGA ACT GAG ATA AAA CCA GGA CAA AAT			8262
Val Asp Ala Pro Asp Gln Lys Gly Thr Glu Ile Lys Pro Gly Gln Asn			
2730	2735	2740	
AAT CCT GTC CCT GTA TCA GAG ACT AAT GAA AGT CCT ATA GTG GAA CGT			8310
Asn Pro Val Pro Val Ser Glu Thr Asn Glu Ser Pro Ile Val Glu Arg			
2745	2750	2755	
ACC CCA TTC AGT TCT AGC AGC TCA AGC AAA CAC AGT TCA CCT AGT GGG			8358
Thr Pro Phe Ser Ser Ser Ser Ser Lys His Ser Ser Pro Ser Gly			
2760	2765	2770	2775
ACT GTT GCT GCC AGA GTG ACT CCT TTT AAT TAC AAC CCA AGC CCT AGG			8406
Thr Val Ala Ala Arg Val Thr Pro Phe Asn Tyr Asn Pro Ser Pro Arg			
2780	2785	2790	
AAA AGC AGC GCA GAT AGC ACT TCA GCT CGG CCA TCT CAG ATC CCA ACT			8454
Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg Pro Ser Gln Ile Pro Thr			
2795	2800	2805	
CCA GTG AAT AAC ACA AAG AAG CGA GAT TCC AAA ACT GAC AGC ACA			8502
Pro Val Asn Asn Asn Thr Lys Lys Arg Asp Ser Lys Thr Asp Ser Thr			
2810	2815	2820	
GAA TCC AGT GGA ACC CAA AGT CCT AAG CGC CAT TCT GGG TCT TAC CTT			8550
Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg His Ser Gly Ser Tyr Leu			
2825	2830	2835	
GTG ACA TCT GTT TAAAAGAGAG GAAGAATGAA ACTAAGAAAA TTCTATGTTA			8602
Val Thr Ser Val			
2840			
ATTACAAC TG CTATATAGAC ATTTTGTTTC AAATGAAACT TTAAAAGACT GAAAAATT TT			8662
GTAAATAGGT TTGATTCTTG TTAGAGGGTT TTTGTTCTGG AAGCCATATT TGATAGTATA			8722
CTTGTCTTC ACTGGTCTTA TTTTGGGAGG CACTCTTGAT GGTTAGGAAA AAATAGAAAG			8782
CCAAGTATGT TTGTACAGTA TGTTTACAT GTATTAAAG TAGCATCCCA TCCCAACTTC			8842
CTTAATTATT GCTTGCTAA AATAATGAAC ACTACAGATA GGAAATATGA TATATTGCTG			8902
TTATCAATCA TTTCTAGATT ATAAACTGAC TAAACTTACA TCAGGGAAA ATTGGTATTT			8962

ATGCAAAAAA AAAATGTTT TGTCCTTGTG AGTCCATCTA ACATCATAAT TAATCATGTG	9022
GCTGTGAAAT TCACAGTAAT ATGGTCCCCG ATGAACAAGT TTACCCAGCC TGCTTGCTT	9082
ACTGCATGAA TGAAACTGAT GGTTCAATT CAGAAGTAAT GATTAACAGT TATGTGGTCA	9142
CATGATGTGC ATAGAGATAG CTACAGTGT AATAATTACA CTATTTGTG CTCCAAACAA	9202
AACAAAAATC TGTGTAAC TG TAAAACATTG AATGAAACTA TTTTACCTGA ACTAGATTT	9262
ATCTGAAAGT AGGTAGAATT TTTGCTATGC TGTAAATTGT TGTATATTCT GGTATTTGAG	9322
GTGAGATGGC TGCTTTAT TAATGAGACA TGAATTGTGT CTCAACAGAA ACTAAATGAA	9382
CATTTCAGAA TAAATTATTG CTGTATGTAA ACTGTTACTG AAATTGGTAT TTGTTTGAAG	9442
GGTTTGTTC ACATTTGTAT TAATTAATTG TTTAAAATGC CTCTTTAAA AGCTTATATA	9502
AATTTTTCT TCAGCTTCTA TGCATTAAGA GTAAAATTCC TCTTACTGT AAAAAAACAT	9562
TGAAGAAGAC TGTGCCCCACT TAACCATTCC ATGCGTTGGC ACTT	9606

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2843 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: protein
  - xii) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu																
1	5													10	15	
Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn																
	20													25	30	
His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu																
	35													40	45	
Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly																
	50													55	60	
Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser																
	65													70	75	80
Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr																
	85													90	95	

Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro  
                   100                     105                     110  
  
 Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg  
                   115                     120                     125  
  
 Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu  
                   130                     135                     140  
  
 Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala  
                   145                     150                     155                     160  
  
 Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu  
                   165                     170                     175  
  
 Asn Phe Ser Leu Gln Thr Asp Leu Thr Arg Arg Gln Leu Glu Tyr Glu  
                   180                     185                     190  
  
 Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln  
                   195                     200                     205  
  
 Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile  
                   210                     215                     220  
  
 Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr  
                   225                     230                     235                     240  
  
 Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp  
                   245                     250                     255  
  
 Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala  
                   260                     265                     270  
  
 Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr  
                   275                     280                     285  
  
 Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu  
                   290                     295                     300  
  
 Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser  
                   305                     310                     315                     320  
  
 Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala  
                   325                     330                     335  
  
 Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys  
                   340                     345                     350  
  
 Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val  
                   355                     360                     365

Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser  
 370 375 380  
 Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly  
 385 390 395 400  
 Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr  
 405 410 415  
 Cys Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp  
 420 425 430  
 Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro  
 435 440 445  
 Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His  
 450 455 460  
 Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln  
 465 470 475 480  
 Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr  
 485 490 495  
 Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp  
 500 505 510  
 Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala  
 515 520 525  
 Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile  
 530 535 540  
 Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys  
 545 550 555 560  
 Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala  
 565 570 575  
 Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu  
 580 585 590  
 Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala  
 595 600 605  
 Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser  
 610 615 620  
 Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Ile Leu Arg  
 625 630 635 640

Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu		
645	650	655
Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His		
660	665	670
Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser		
675	680	685
Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val		
690	695	700
Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met		
705	710	715
Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys		
725	730	735
Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu		
740	745	750
His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His		
755	760	765
Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser		
770	775	780
His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val		
785	790	795
Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr		
805	810	815
Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro		
820	825	830
Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys		
835	840	845
Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His		
850	855	860
Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile		
865	870	880
Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala		
885	890	895
Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu		
900	905	910

His	Cys	Val	Thr	Asp	Glu	Arg	Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala
915					920					925					
His	Thr	His	Ser	Asn	Thr	Tyr	Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn
930					935					940					
Arg	Thr	Cys	Ser	Met	Pro	Tyr	Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser
945					950					955			960		
Asn	Asp	Ser	Leu	Asn	Ser	Val	Ser	Ser	Asn	Asp	Gly	Tyr	Gly	Lys	Arg
						965			970			975			
Gly	Gln	Met	Lys	Pro	Ser	Ile	Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser
						980			985			990			
Lys	Phe	Cys	Ser	Tyr	Gly	Gln	Tyr	Pro	Ala	Asp	Leu	Ala	His	Lys	Ile
						995			1000			1005			
His	Ser	Ala	Asn	His	Met	Asp	Asp	Asn	Asp	Gly	Glu	Leu	Asp	Thr	Pro
						1010			1015			1020			
Ile	Asn	Tyr	Ser	Leu	Lys	Tyr	Ser	Asp	Glu	Gln	Leu	Asn	Ser	Gly	Arg
1025					1030					1035			1040		
Gln	Ser	Pro	Ser	Gln	Asn	Glu	Arg	Trp	Ala	Arg	Pro	Lys	His	Ile	Ile
						1045			1050			1055			
Glu	Asp	Glu	Ile	Lys	Gln	Ser	Glu	Gln	Arg	Gln	Ser	Arg	Asn	Gln	Ser
						1060			1065			1070			
Thr	Thr	Tyr	Pro	Val	Tyr	Thr	Glu	Ser	Thr	Asp	Asp	Lys	His	Leu	Lys
						1075			1080			1085			
Phe	Gln	Pro	His	Phe	Gly	Gln	Gln	Glu	Cys	Val	Ser	Pro	Tyr	Arg	Ser
						1090			1095			1100			
Arg	Gly	Ala	Asn	Gly	Ser	Glu	Thr	Asn	Arg	Val	Gly	Ser	Asn	His	Gly
						1105			1110			1115			1120
Ile	Asn	Gln	Asn	Val	Ser	Gln	Ser	Leu	Cys	Gln	Glu	Asp	Asp	Tyr	Glu
						1125			1130			1135			
Asp	Asp	Lys	Pro	Thr	Asn	Tyr	Ser	Glu	Arg	Tyr	Ser	Glu	Glu	Gln	
						1140			1145			1150			
His	Glu	Glu	Glu	Glu	Arg	Pro	Thr	Asn	Tyr	Ser	Ile	Lys	Tyr	Asn	Glu
						1155			1160			1165			
Glu	Lys	Arg	His	Val	Asp	Gln	Pro	Ile	Asp	Tyr	Ser	Leu	Lys	Tyr	Ala
						1170			1175			1180			

Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser  
 1185 1190 1195 1200  
 Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu  
 1205 1210 1215  
 Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His  
 1220 1225 1230  
 Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr  
 1235 1240 1245  
 Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val  
 1250 1255 1260  
 Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu  
 1265 1270 1275 1280  
 Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala  
 1285 1290 1295  
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Gly Lys Ile Gly  
 1300 1305 1310  
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln  
 1315 1320 1325  
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser  
 1330 1335 1340  
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Pro Ser Gly Ala Lys Ser  
 1345 1350 1355 1360  
 Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr  
 1365 1370 1375  
 Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser  
 1380 1385 1390  
 Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu  
 1395 1400 1405  
 Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro  
 1410 1415 1420  
 Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro  
 1425 1430 1435 1440  
 Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys  
 1445 1450 1455

Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val  
 1460 1465 1470  
  
 Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu  
 1475 1480 1485  
  
 Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser  
 1490 1495 1500  
  
 Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val  
 1505 1510 1515 1520  
  
 Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu  
 1525 1530 1535  
  
 Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu  
 1540 1545 1550  
  
 Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp  
 1555 1560 1565  
  
 Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro  
 1570 1575 1580  
  
 Thr Lys Ser Ser Arg Lys Gly Lys Lys Pro Ala Gln Thr Ala Ser Lys  
 1585 1590 1595 1600  
  
 Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys  
 1605 1610 1615  
  
 Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe  
 1620 1625 1630  
  
 Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro  
 1635 1640 1645  
  
 Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser  
 1650 1655 1660  
  
 Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln  
 1665 1670 1675 1680  
  
 Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser  
 1685 1690 1695  
  
 Thr Asp Glu Ala Gln Gly Lys Thr Ser Ser Val Thr Ile Pro Glu  
 1700 1705 1710  
  
 Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile  
 1715 1720 1725

Asn	Ser	Ala	Met	Pro	Lys	Gly	Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys
1730					1735					1740					
Lys	Ile	Met	Asp	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro
1745					1750					1755					1760
Asn	Lys	Asn	Gln	Leu	Asp	Gly	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val	
					1765			1770						1775	
Lys	Pro	Ile	Pro	Gln	Asn	Thr	Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys	Asn
					1780			1785						1790	
Ala	Asp	Ser	Lys	Asn	Asn	Leu	Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn
					1795			1800						1805	
Lys	Asp	Ser	Lys	Lys	Gln	Asn	Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn
					1810			1815						1820	
Asp	Lys	Leu	Pro	Asn	Asn	Glu	Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe
					1825			1830						1835	
Asp	Ser	Pro	His	His	Tyr	Thr	Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe
					1845			1850						1855	
Ser	Arg	Asn	Asp	Ser	Leu	Ser	Ser	Leu	Asp	Phe	Asp	Asp	Asp	Asp	Val
					1860			1865						1870	
Asp	Leu	Ser	Arg	Glu	Lys	Ala	Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys
					1875			1880						1885	
Glu	Ser	Glu	Ala	Lys	Val	Thr	Ser	His	Thr	Glu	Leu	Thr	Ser	Asn	Gln
					1890			1895						1900	
Gln	Ser	Ala	Asn	Lys	Thr	Gln	Ala	Ile	Ala	Lys	Gln	Pro	Ile	Asn	Arg
					1905			1910						1915	
Gly	Gln	Pro	Lys	Pro	Ile	Leu	Gln	Lys	Gln	Ser	Thr	Phe	Pro	Gln	Ser
					1925			1930						1935	
Ser	Lys	Asp	Ile	Pro	Asp	Arg	Gly	Ala	Ala	Thr	Asp	Glu	Lys	Leu	Gln
					1940			1945						1950	
Asn	Phe	Ala	Ile	Glu	Asn	Thr	Pro	Val	Cys	Phe	Ser	His	Asn	Ser	Ser
					1955			1960						1965	
Leu	Ser	Ser	Leu	Ser	Asp	Ile	Asp	Gln	Glu	Asn	Asn	Asn	Lys	Glu	Asn
					1970			1975						1980	
Glu	Pro	Ile	Lys	Glu	Thr	Glu	Pro	Pro	Asp	Ser	Gln	Gly	Glu	Pro	Ser
					1985			1990						1995	
															2000

Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp  
 2005 2010 2015

Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile  
 2020 2025 2030

Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro  
 2035 2040 2045

Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser  
 2050 2055 2060

Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu  
 2065 2070 2075 2080

Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser  
 2085 2090 2095

Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val  
 2100 2105 2110

Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala  
 2115 2120 2125

Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu  
 2130 2135 2140

Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr  
 2145 2150 2155 2160

Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu  
 2165 2170 2175

Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys  
 2180 2185 2190

Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu  
 2195 2200 2205

Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile  
 2210 2215 2220

Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser  
 2225 2230 2235 2240

Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro  
 2245 2250 2255

Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg  
 2260 2265 2270

Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln  
2275 2280 2285

Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser  
2290 2295 2300

Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro  
2305 2310 2315 2320

Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile  
2325 2330 2335

Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser  
2340 2345 2350

Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser  
2355 2360 2365

Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu  
2370 2375 2380

Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly  
2385 2390 2395 2400

Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu  
2405 2410 2415

Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser  
2420 2425 2430

Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro  
2435 2440 2445

Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser  
2450 2455 2460

Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln  
2465 2470 2475 2480

Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His  
2485 2490 2495

Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser  
2500 2505 2510

Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile  
2515 2520 2525

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser  
2530 2535 2540

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg  
 2545 2550 2555 2560  
 Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala  
 2565 2570 2575  
 Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val  
 2580 2585 2590  
 Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala  
 2595 2600 2605  
 Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn  
 2610 2615 2620  
 Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser  
 2625 2630 2635 2640  
 Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp  
 2645 2650 2655  
 Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly  
 2660 2665 2670  
 Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu  
 2675 2680 2685  
 Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln  
 2690 2695 2700  
 Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn  
 2705 2710 2715 2720  
 Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr  
 2725 2730 2735  
 Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn  
 2740 2745 2750  
 Glu Ser Pro Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser  
 2755 2760 2765  
 Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe  
 2770 2775 2780  
 Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala  
 2785 2790 2795 2800  
 Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg  
 2805 2810 2815

Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys  
2820 2825 2830

Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val  
2835 2840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DP1(TB2)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCA GTC GCC GCT CCA GTC TAT CCG GCA CTA GGA ACA GCC CCG GGN GGC	48
Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly	
1 5 10 15	
GAG ACG GTC CCC GCC ATG TCT GCG GCC ATG AGG GAG AGG TTC GAC CGG	96
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg	
20 25 30	
TTC CTG CAC GAG AAG AAC TGC ATG ACT GAC CTT CTG GCC AAG CTC GAG	144
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu	
35 40 45	
GCC AAA ACC GGC GTG AAC AGG AGC TTC ATC GCT CTT GGT GTC ATC GGA	192
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly	
50 55 60	
CTG GTG GCC TTG TAC CTG GTG TTC GGT TAT GGA GCC TCT CTC CTC TGC	240
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys	
65 70 75 80	
AAC CTG ATA GGA TTT GGC TAC CCA GCC TAC ATC TCA ATT AAA GCT ATA	288

Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile			
85	90	95	
GAG AGT CCC AAC AAA GAA GAT GAT ACC CAG TGG CTG ACC TAC TGG GTA			336
Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val			
100	105	110	
GTG TAT GGT GTG TTC AGC ATT GCT GAA TTC TTC TCT GAT ATC TTC CTG			384
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu			
115	120	125	
TCA TGG TTC CCC TTC TAC TAC ATG CTG AAG TGT GGC TTC CTG TTG TGG			432
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp			
130	135	140	
TGC ATG GCC CCG AGC CCT TCT AAT GGG GCT GAA CTG CTC TAC AAG CGC			480
Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg			
145	150	155	160
ATC ATC CGT CCT TTC CTG AAG CAC GAG TCC CAG ATG GAC AGT GTG			528
Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val			
165	170	175	
GTC AAG GAC CTT AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT			576
Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr			
180	185	190	
AAA GAA GCG AAG AAA GCT ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG			624
Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys			
195	200	205	
AGC ACC TAAACCAGAC TAAACCAGAC TGGATGGAAA CTTCCCTGCC CTCCTGTACC			680
Ser Thr			
210			
TTCCCTACTGG AGCTTGATGT TATATTAGGG ACTGTGGTAT AATTATTTA ATAATGTTGC			740
CTTGGAAACA TTTTGAGAT ATTAAAGATT GGAATGTGTT GTAAGTTCT TTGCTTACTT			800
TTACTGTCTA TATATATAGG GAGCACTTTA AACTTAATGC AGTGGGCAGT GTCCACGTTT			860
TTGGAAAATG TATTTGCCT CTGGGTAGGA AAAGATGTAT GTTGCTATCC TGCAGGAAAT			920
ATAAAACTAA AATAAAATTA TATACCCCAC AGGCTGTGTA CTTTACTGGG CTCTCCCTGC			980
ACGSATTTTC TCTGTAGTTA CATTAGGRT AATCTTATG GTTCTACTTC CTRTAATGTA			1040
CAATTTATA TAATTCNGRA ATGTTTTAA TGTATTTGTG CACATGTACA TATGGAAATG			1100
TTACTGTCTG ACTACANCAT GCATCATGCT CATGGGGAGG GAGCAGGGGA AGGTTGTATG			1160

TGTCATTTAT	AACTTCTGTA	CAGTAAGACC	ACCTGCCAAA	AGCTGGAGGA	ACCATTGTGC	1220
TGGTGTGGTC	TACTAAATAA	TACTTTAGGA	AATACGTGAT	TAATATGCAA	GTGAACAAAG	1280
TGAGAAATGA	AATCGAATGG	AGATTGGCCT	GGTTGTTCC	GTAGTATATG	GCATATGAAT	1340
ACCAGGATAG	CTTTATAAAG	CAGTTAGTTA	GTTAGTTACT	CACTCTAGTG	ATAAATCGGG	1400
AAATTTACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAG	1460
AGTACCCCTGT	AACTCTCAAT	TCCCTGAAAAA	ACTAGTAATA	CTGTCTTATC	TGCTATAAAC	1520
TTTACATATT	TGTCTATTGT	CAAGATGCTA	CANTGGAMNC	CATTTCTGGT	TTTATCTTCA	1580
NAGSGGAGAN	ACATGTTGAT	TTAGTCTTCT	TTCCCAATCT	TCTTTTTAA	MCCAGTTTNA	1640
GGMNCTTCTG	RAGATTGYC	CACCTCTGAT	TACATGTATG	TTCTYGTGG	TATCATKAGC	1700
AACAACATGC	TAATGRGCAC	ACCTAGCTCT	RAGMGCAATT	CTGGGAGANT	GARAGGNWGT	1760
ATARAGTMNC	CCATAATCTG	CTTGGCAATA	GTAAAGTCAA	TCTATCTTCA	GTTCCTCTCT	1820
GGCCTTTAAG	GTCAAACACA	AGAGGCTTCC	CTAGTTACA	AGTCAGAGTC	ACTTGTAGTC	1880
CATTTAAATG	CCCTCATCCG	TATTCTTGT	GTTGATAAGC	TGCACAKGAC	TACATAGTAA	1940
GTACAGANCA	GTAAAGTTAA	NNCGGATGTC	TCCATTGATC	TGCCAANTCG	NTATAGAGAG	2000
CAATTGTCT	GGACTAGAAA	ATCTGAGTTT	TACACCATAAC	TGTTAAGAGT	CCTTTGAAT	2060
TAAACTAGAC	TAAAACAAGT	GTATAACTAA	ACTAACAAAGA	TTAAATATCC	AGCCAGTACA	2120
GTATTTTTA	AGGCAAATAA	AGATGATTAG	CTCACCTTGA	GNTAACAAATC	AGGTAAGATC	2180
ATNACAATGT	CTCATGATGT	NAANAATATT	AAAGATATCA	ATACTAAGTG	ACAGTATCAC	2240
NNCTAATATA	ATATGGATCA	GAGCATTAT	TTTGGGGAGG	AAAACAGTGG	TGATTACCGG	2300
CATTTATTAA	AACTAAAAC	TTGTAGAAA	GCAAACAAAA	TTGTTCTTGG	GAGAAAATCA	2360
ACTTTAGAT	AAAAAAATT	TTAAGTAWCT	AGGAGTATTT	AAATCCTTT	CCCATAAATA	2420
AAAGTACAGT	TTCTGGTG	GCAGAATGAA	AATCAGCAAC	NTCTAGCATA	TAGACTATAT	2480
AATCAGATTG	ACAGCATATA	GAATATATTA	TCAGACAAGA	TGAGGAGGTA	CAAAAGTTAC	2540
TATTGCTCAT	AATGACTTAC	AGGCTAAAAN	TAGNTNTAAA	ATACTATATT	AAATTCTGAA	2600
TGCAATTTT	TTTGTTCCC	TTGAGACCAA	AATTAAAGTT	AACTGTTGCT	GGCAGTCTAA	2660
GTGTAAATGT	TAACAGCAGG	AGAAGTTAAG	AATTGAGCAG	TTCTGTTGCA	TGATTTCCCA	2720

AATGAAATAC TGCCTGGCT AGAGTTGAA AAACTAATTG AGCCTGTGCC	TGGCTAGAAA	2780
ACAAGCGTTT ATTTGAATGT GAATAGTGTT TCAAAGGTAT GTAGTTACAG AATT CCTACC		2840
AAACAGCTTA AATTCTCAA GAAAGAATTG CTGCAGCAGT TATTCCCTTA CCTGAAGGCT		2900
TCAATCATTG GGATCAACAA CTGCTACTCT CGGGAAGACT CCTCTACTCA CAGCTGAAGA		2960
AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATCCTGAA GATGTGATAC ACTGAATGGA		3020
AATAAAATAGA TGAAATAAA ATTGAGWTCT CATTAAAAAA AAACCATGTG CCCAATGGGA		3080
AAATGACCTC ATGTTGTGGT TTAAACAGCA ACTGCACCCA CTAGCACAGC CCATTGAGCT		3140
ANCCTATATA TACATCTCTG TCAGTGCCCC TC		3172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly			
1	5	10	15
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg			
20	25	30	
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu			
35	40	45	
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly			
50	55	60	
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys			
65	70	75	80
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile			
85	90	95	
Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val			
100	105	110	
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu			

115	120	125
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp		
130	135	140
Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg		
145	150	155
Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val		
165	170	175
Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr		
180	185	190
Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys		
195	200	205
Ser Thr		
210		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 434 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 

- (B) CLONE: TB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Ala Pro Val Val Val Gly Ser Gly Arg Ala Pro Arg His Pro Ala			
1	5	10	15

Pro Ala Ala Met His Pro Arg Arg Pro Asp Gly Phe Asp Gly Leu Gly			
20	25	30	

Tyr Arg Gly Gly Ala Arg Asp Glu Gln Gly Phe Gly Gly Ala Phe Pro			
35	40	45	

Ala Arg Ser Phe Ser Thr Gly Ser Asp Leu Gly His Trp Val Thr Thr			
50	55	60	

Pro	Pro	Asp	Ile	Pro	Gly	Ser	Arg	Asn	Leu	His	Trp	Gly	Glu	Lys	Ser
65					70					75				80	
Pro	Pro	Tyr	Gly	Val	Pro	Thr	Thr	Ser	Thr	Pro	Tyr	Glu	Gly	Pro	Thr
		85						90						95	
Glu	Glu	Pro	Phe	Ser	Ser	Gly	Gly	Gly	Ser	Val	Gln	Gly	Gln	Ser	
		100				105					110				
Ser	Glu	Gln	Leu	Asn	Arg	Phe	Ala	Gly	Phe	Gly	Ile	Gly	Leu	Ala	Ser
	115					120					125				
Leu	Phe	Thr	Glu	Asn	Val	Leu	Ala	His	Pro	Cys	Ile	Val	Leu	Arg	Arg
	130					135					140				
Gln	Cys	Gln	Val	Asn	Tyr	His	Ala	Gln	His	Tyr	His	Leu	Thr	Pro	Phe
	145					150				155			160		
Thr	Val	Ile	Asn	Ile	Met	Tyr	Ser	Phe	Asn	Lys	Thr	Gln	Gly	Pro	Arg
		165						170				175			
Ala	Leu	Trp	Lys	Gly	Met	Gly	Ser	Thr	Phe	Ile	Val	Gln	Gly	Val	Thr
	180						185					190			
Leu	Gly	Ala	Glu	Gly	Ile	Ile	Ser	Glu	Phe	Thr	Pro	Leu	Pro	Arg	Glu
	195						200					205			
Val	Leu	His	Lys	Trp	Ser	Pro	Lys	Gln	Ile	Gly	Glu	His	Leu	Leu	Leu
	210					215					220				
Lys	Ser	Leu	Thr	Tyr	Val	Val	Ala	Met	Pro	Phe	Tyr	Ser	Ala	Ser	Leu
	225					230				235			240		
Ile	Glu	Thr	Val	Gln	Ser	Glu	Ile	Ile	Arg	Asp	Asn	Thr	Gly	Ile	Leu
		245					250					255			
Glu	Cys	Val	Lys	Glu	Gly	Ile	Gly	Arg	Val	Ile	Gly	Met	Gly	Val	Pro
		260					265					270			
His	Ser	Lys	Arg	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Ile	Phe	Pro	Thr	Val
		275					280					285			
Leu	His	Gly	Val	Leu	His	Tyr	Ile	Ile	Ser	Ser	Val	Ile	Gln	Lys	Phe
	290						295				300				
Val	Leu	Leu	Ile	Leu	Lys	Arg	Lys	Thr	Tyr	Asn	Ser	His	Leu	Ala	Glu
	305					310				315			320		
Ser	Thr	Ser	Pro	Val	Gln	Ser	Met	Leu	Asp	Ala	Tyr	Phe	Pro	Glu	Leu
				325					330			335			

Ile Ala Asn Phe Ala Ala Ser Leu Cys Ser Asp Val Ile Leu Tyr Pro  
                  340                     345                 350  
  
 Leu Glu Thr Val Leu His Arg Leu His Ile Gln Gly Thr Arg Thr Ile  
                  355                     360                 365  
  
 Ile Asp Asn Thr Asp Leu Gly Tyr Glu Val Leu Pro Ile Asn Thr Gln  
                  370                     375                 380  
  
 Tyr Glu Gly Met Arg Asp Cys Ile Asn Thr Ile Arg Gln Glu Glu Gly  
                  385                     390                 395                 400  
  
 Val Phe Gly Phe Tyr Lys Gly Phe Gly Ala Val Ile Ile Gln Tyr Thr  
                  405                     410                 415  
  
 Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu  
                  420                     425                 430  
  
 Leu Gln

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: YS-39(TB2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Leu Arg Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr  
  1                 5                     10                 15  
  
 Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe  
  20                 25                     30  
  
 Ile Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly  
  35                 40                     45

Tyr	Gly	Ala	Ser	Leu	Leu	Cys	Asn	Leu	Ile	Gly	Phe	Gly	Tyr	Pro	Ala
50															60
Tyr	Ile	Ser	Ile	Lys	Ala	Ile	Glu	Ser	Pro	Asn	Lys	Glu	Asp	Asp	Thr
65															80
Gln	Trp	Leu	Thr	Tyr	Trp	Val	Val	Tyr	Gly	Val	Phe	Ser	Ile	Ala	Glu
															95
85															
Phe	Phe	Ser	Asp	Ile	Phe	Leu	Ser	Trp	Phe	Pro	Phe	Tyr	Tyr	Ile	Leu
															100
															105
															110
Lys	Cys	Gly	Phe	Leu	Leu	Trp	Cys	Met	Ala	Pro	Ser	Pro	Ser	Asn	Gly
															115
															120
															125
Ala	Glu	Leu	Leu	Tyr	Lys	Arg	Ile	Ile	Arg	Pro	Phe	Phe	Leu	Lys	His
															130
															135
															140
Glu	Ser	Gln	Met	Asp	Ser	Val	Val	Lys	Asp	Leu	Lys	Asp	Lys	Ala	Lys
															145
															150
															155
															160
Glu	Thr	Ala	Asp	Ala	Ile	Thr	Lys	Glu	Ala	Lys	Lys	Ala	Thr	Val	Asn
															165
															170
															175
Leu	Leu	Gly	Glu	Glu	Lys	Lys	Ser	Thr							
															180
															185

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: [2842] 2843 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 

- (B) CLONE: APC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Ala	Ala	Ser	Tyr	Asp	Gln	Leu	Leu	Lys	Gln	Val	Glu	Ala	Leu
1	'														15

Lys	Met	Glu	Asn	Ser	Asn	Leu	Arg	Gln	Glu	Leu	Glu	Asp	Asn	Ser	Asn

20

25

30

His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu  
 35 40 45

Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly  
 50 55 60

Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser  
 65 70 75 80

Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr  
 85 90 95

Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro  
 100 105 110

Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg  
 115 120 125

Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu  
 130 135 140

Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala  
 145 150 155 160

Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu [Leu Thr Glu Asn  
 165 170 175

Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala  
 180 185 190

Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln Asp  
 195 200 205

Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu  
 210 215 220

Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu  
 225 230 235 240

Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala  
 245 250 255

Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr  
 260 265 270

Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala  
 275 280 285

Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr  
 290 295 300

Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met  
 305                    310                    315                    320  
  
 Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met  
 325                    330                    335  
  
 Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys Leu  
 340                    345                    350  
  
 Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val Leu  
 355                    360                    365  
  
 Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala  
 370                    375                    380  
  
 Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly Arg  
 385                    390                    395                    400  
  
 Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr Cys  
 405                    410                    415  
  
 Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp Gln  
 420                    425                    430  
  
 Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro Ala  
 435                    440                    445  
  
 Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His Ala  
 450                    455                    460  
  
 Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln Val  
 465                    470                    475                    480  
  
 Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr Leu  
 485                    490                    495  
  
 Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp Val  
 500                    505                    510  
  
 Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala Leu  
 515                    520                    525  
  
 Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile Ala  
 530                    535                    540  
  
 Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys Lys  
 545                    550                    555                    560  
  
 Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala Leu  
 565                    570                    575  
  
 Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu Trp  
 580                    585                    590

Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala Val  
 595 600 605  
 Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln  
 610 615 620  
 Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Ile Leu Arg Asn  
 625 630 635 640  
 Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu Arg  
 645 650 655  
 Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His Ser  
 660 665 670  
 Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala  
 675 680 685  
 Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser  
 690 695 700  
 Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly  
 705 710 715 720  
 Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr  
 725 730 735  
 Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His  
 740 745 750  
 Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu  
 755 760 765  
 Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His  
 770 775 780  
 Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe  
 785 790 795 800  
 Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly  
 805 810 815  
 Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser  
 820 825 830  
 Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp  
 835 840 845  
 Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro  
 850 855 860  
 Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser  
 865 870 875 880

Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile  
                   885                  890                  895  
  
 His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His  
                   900                  905                  910  
  
 Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His  
                   915                  920                  925  
  
 Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg  
                   930                  935                  940  
  
 Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn  
                   945                  950                  955                  960  
  
 Asp Ser Leu Asn Ser Val Ser Ser Asp Gly Tyr Gly Lys Arg Gly  
                   965                  970                  975  
  
 Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys  
                   980                  985                  990  
  
 Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile His  
                   995                  1000                  1005  
  
 Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile  
                   1010                  1015                  1020  
  
 Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln  
                   1025                  1030                  1035                  1040  
  
 Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile Glu  
                   1045                  1050                  1055  
  
 Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr  
                   1060                  1065                  1070  
  
 Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys Phe  
                   1075                  1080                  1085  
  
 Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg  
                   1090                  1095                  1100  
  
 Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly Ile  
                   1105                  1110                  1115                  1120  
  
 Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp  
                   1125                  1130                  1135  
  
 Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln His  
                   1140                  1145                  1150  
  
 Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu  
                   1155                  1160                  1165

Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr  
 1170 1175 1180

Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser  
 1185 1190 1195 1200

Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu Asn  
 1205 1210 1215

Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro  
 1220 1225 1230

Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys  
 1235 1240 1245

Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu  
 1250 1255 1260

Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser  
 1265 1270 1275 1280

Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp  
 1285 1290 1295

Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly Thr  
 1300 1305 1310

Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His  
 1315 1320 1325

Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu  
 1330 1335 1340

Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro  
 1345 1350 1355 1360

Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val  
 1365 1370 1375

Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu  
 1380 1385 1390

Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro  
 1395 1400 1405

Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp  
 1410 1415 1420

Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro  
 1425 1430 1435 1440

Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala  
 1445 1450 1455

Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn  
                  1460                 1465                 1470  
  
 Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu  
                  1475                 1480                 1485  
  
 His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser  
                  1490                 1495                 1500  
  
 Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val Glu  
                  1505                 1510                 1515                 1520  
  
 Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr  
                  1525                 1530                 1535  
  
 Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala  
                  1540                 1545                 1550  
  
 Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp  
                  1555                 1560                 1565  
 Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr  
                  1570                 1575                 1580  
  
 Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu  
                  1585                 1590                 1595                 1600  
  
 Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu  
                  1605                 1610                 1615  
  
 Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr  
                  1620                 1625                 1630  
  
 Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro Ile  
                  1635                 1640                 1645  
  
 Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro  
                  1650                 1655                 1660  
  
 Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln Ser  
                  1665                 1670                 1675                 1680  
  
 Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr  
                  1685                 1690                 1695  
  
 Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu Leu  
                  1700                 1705                 1710  
  
 Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn  
                  1715                 1720                 1725  
  
 Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys Lys  
                  1730                 1735                 1740

Ile	Met	Asp	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro	Asn
1745				1750					1755				1760		
Lys	Asn	Gln	Leu	Asp	Gly	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val	Lys	
				1765				1770				1775			
Pro	Ile	Pro	Gln	Asn	Thr	Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys	Asn	Ala
					1780			1785			1790				
Asp	Ser	Lys	Asn	Asn	Leu	Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn	Lys
					1795			1800			1805				
Asp	Ser	Lys	Lys	Gln	Asn	Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn	Asp
					1810			1815			1820				
Lys	Leu	Pro	Asn	Asn	Glu	Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe	Asp
					1825			1830			1835			1840	
Ser	Pro	His	His	Tyr	Thr	Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe	Ser
					1845			1850			1855				
Arg	Asn	Asp	Ser	Leu	Ser	Ser	Leu	Asp	Phe	Asp	Asp	Asp	Asp	Val	Asp
					1860			1865			1870				
Leu	Ser	Arg	Glu	Lys	Ala	Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys	Glu
					1875			1880			1885				
Ser	Glu	Ala	Lys	Val	Thr	Ser	His	Thr	Glu	Leu	Thr	Ser	Asn	Gln	Gln
					1890			1895			1900				
Ser	Ala	Asn	Lys	Thr	Gln	Ala	Ile	Ala	Lys	Gln	Pro	Ile	Asn	Arg	Gly
					1905			1910			1915			1920	
Gln	Pro	Lys	Pro	Ile	Leu	Gln	Lys	Gln	Ser	Thr	Phe	Pro	Gln	Ser	Ser
					1925			1930			1935				
Lys	Asp	Ile	Pro	Asp	Arg	Gly	Ala	Ala	Thr	Asp	Glu	Lys	Leu	Gln	Asn
					1940			1945			1950				
Phe	Ala	Ile	Glu	Asn	Thr	Pro	Val	Cys	Phe	Ser	His	Asn	Ser	Ser	Leu
					1955			1960			1965				
Ser	Ser	Leu	Ser	Asp	Ile	Asp	Gln	Glu	Asn	Asn	Asn	Lys	Glu	Asn	Glu
					1970			1975			1980				
Pro	Ile	Lys	Glu	Thr	Glu	Pro	Pro	Asp	Ser	Gln	Gly	Glu	Pro	Ser	Lys
					1985			1990			1995			2000	
Pro	Gln	Ala	Ser	Gly	Tyr	Ala	Pro	Lys	Ser	Phe	His	Val	Glu	Asp	Thr
					2005			2010			2015				
Pro	Val	Cys	Phe	Ser	Arg	Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ile	Asp
					2020			2025			2030				

Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys  
 2035 2040 2045  
 Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro  
 2050 2055 2060  
 Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys  
 2065 2070 2075 2080  
 Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu  
 2085 2090 2095  
 Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser  
 2100 2105 2110  
 Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser  
 2115 2120 2125  
 Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly  
 2130 2135 2140  
 Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser  
 2145 2150 2155 2160  
 Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu  
 2165 2170 2175  
 Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys  
 2180 2185 2190  
 Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile  
 2195 2200 2205  
 Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser  
 2210 2215 2220  
 Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser  
 2225 2230 2235 2240  
 Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala  
 2245 2250 2255  
 Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly  
 2260 2265 2270  
 Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln Thr  
 2275 2280 2285  
 Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg  
 2290 2295 2300  
 Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile

2305	2310	2315	2320
Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser			
2325		2330	2335
Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr			
2340		2345	2350
Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro			
2355		2360	2365
Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser			
2370		2375	2380
Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu			
2385	2390	2395	2400
Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser			
2405		2410	2415
Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu			
2420		2425	2430
Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser			
2435		2440	2445
Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu			
2450		2455	2460
Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr			
2465	2470	2475	2480
Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser			
2485		2490	2495
Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro			
2500		2505	2510
Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala			
2515		2520	2525
Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly			
2530		2535	2540
Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val			
2545	2550	2555	2560
Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser			
2565		2570	2575
Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn			
2580		2585	2590
Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys			

2595	2600	2605
Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser		
2610	2615	2620
Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys		
2625	2630	2640
Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val		
2645	2650	2655
Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg		
2660	2665	2670
Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys		
2675	2680	2685
Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn		
2690	2695	2700
Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn Arg		
2705	2710	2715
Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr Glu		
2725	2730	2735
Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn Glu		
2740	2745	2750
Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Lys		
2755	2760	2765
His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe Asn		
2770	2775	2780
Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg		
2785	2790	2800
Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg Asp		
2805	2810	2815
Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg		
2820	2825	2830
His Ser Gly Ser Tyr Leu Val Thr Ser Val		
2835	2840]	

Pro Leu Thr Glu  
175

Asn	Phe	Ser	Leu	Gln	Thr	Asp	Met	Thr	Arg	Arg	Gln	Leu	Glu	Tyr	Glu
			180					185					190		

Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln  
195                   200                   205  
Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile  
210                   215                   220  
Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr  
225                   230                   235                   240  
Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp  
245                   250                   255  
Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala  
260                   265                   270  
Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr  
275                   280                   285  
Ala Ser Val Leu Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu  
290                   295                   300  
Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser  
305                   310                   315                   320  
Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala  
325                   330                   335  
Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys  
340                   345                   350  
Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val  
355                   360                   365  
Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser  
370                   375                   380  
Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly  
385                   390                   395                   400  
Arg Arg Glu Ile Arg Val Leu His Leu Glu Gln Ile Arg Ala Tyr  
405                   410                   415  
Cys Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp  
420                   425                   430  
Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro  
435                   440                   445  
Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His  
450                   455                   460  
Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln  
465                   470                   475                   480

<u>Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr</u>		
485	490	495
<hr/>		
<u>Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp</u>		
500	505	510
<hr/>		
<u>Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala</u>		
515	520	525
<hr/>		
<u>Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile</u>		
530	535	540
<hr/>		
<u>Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys</u>		
545	550	555
<hr/>		
<u>Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala</u>		
565	570	575
<hr/>		
<u>Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu</u>		
580	585	590
<hr/>		
<u>Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala</u>		
595	600	605
<hr/>		
<u>Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser</u>		
610	615	620
<hr/>		
<u>Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Ile Leu Arg</u>		
625	630	635
<hr/>		
<u>Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu</u>		
645	650	655
<hr/>		
<u>Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His</u>		
660	665	670
<hr/>		
<u>Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser</u>		
675	680	685
<hr/>		
<u>Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val</u>		
690	695	700
<hr/>		
<u>Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met</u>		
705	710	715
<hr/>		
<u>Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys</u>		
725	730	735
<hr/>		
<u>Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu</u>		
740	745	750
<hr/>		
<u>His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His</u>		
755	760	765

Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser  
 770 775 780

His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val  
 785 790 795 800

Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr  
 805 810 815

Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro  
 820 825 830

Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys  
 835 840 845

Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His  
 850 855 860

Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile  
 865 870 875 880

Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala  
 885 890 895

Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu  
 900 905 910

His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala  
 915 920 925

His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn  
 930 935 940

Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser  
 945 950 955 960

Asn Asp Ser Leu Asn Ser Val Ser Ser Asp Gly Tyr Gly Lys Arg  
 965 970 975

Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser  
 980 985 990

Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile  
 995 1000 1005

His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro  
 1010 1015 1020

Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg  
 1025 1030 1035 1040

Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile  
 1045 1050 1055

Glu	Asp	Glu	Ile	Lys	Gln	Ser	Glu	Gln	Arg	Gln	Ser	Arg	Asn	Gln	Ser
1060					1065						1070				
Thr	Thr	Tyr	Pro	Val	Tyr	Thr	Glu	Ser	Thr	Asp	Asp	Lys	His	Leu	Lys
1075						1080						1085			
Phe	Gln	Pro	His	Phe	Gly	Gln	Gln	Glu	Cys	Val	Ser	Pro	Tyr	Arg	Ser
1090						1095					1100				
Arg	Gly	Ala	Asn	Gly	Ser	Glu	Thr	Asn	Arg	Val	Gly	Ser	Asn	His	Gly
1105						1110				1115				1120	
Ile	Asn	Gln	Asn	Val	Ser	Gln	Ser	Leu	Cys	Gln	Glu	Asp	Asp	Tyr	Glu
1125						1130					1135				
Asp	Asp	Lys	Pro	Thr	Asn	Tyr	Ser	Glu	Arg	Tyr	Ser	Glu	Glu	Glu	Gln
1140						1145					1150				
His	Glu	Glu	Glu	Glu	Arg	Pro	Thr	Asn	Tyr	Ser	Ile	Lys	Tyr	Asn	Glu
1155						1160					1165				
Glu	Lys	Arg	His	Val	Asp	Gln	Pro	Ile	Asp	Tyr	Ser	Leu	Lys	Tyr	Ala
1170						1175					1180				
Thr	Asp	Ile	Pro	Ser	Ser	Gln	Lys	Gln	Ser	Phe	Ser	Phe	Ser	Lys	Ser
1185						1190				1195				1200	
Ser	Ser	Gly	Gln	Ser	Ser	Lys	Thr	Glu	His	Met	Ser	Ser	Ser	Ser	Glu
1205						1210					1215				
Asn	Thr	Ser	Thr	Pro	Ser	Ser	Asn	Ala	Lys	Arg	Gln	Asn	Gln	Leu	His
1220						1225					1230				
Pro	Ser	Ser	Ala	Gln	Ser	Arg	Ser	Gly	Gln	Pro	Gln	Lys	Ala	Ala	Thr
1235						1240				1245					
Cys	Lys	Val	Ser	Ser	Ile	Asn	Gln	Glu	Thr	Ile	Gln	Thr	Tyr	Cys	Val
1250						1255				1260					
Glu	Asp	Thr	Pro	Ile	Cys	Phe	Ser	Arg	Cys	Ser	Ser	Leu	Ser	Ser	Leu
1265						1270				1275			1280		
Ser	Ser	Ala	Glu	Asp	Glu	Ile	Gly	Cys	Asn	Gln	Thr	Thr	Gln	Glu	Ala
1285						1290					1295				
Asp	Ser	Ala	Asn	Thr	Leu	Gln	Ile	Ala	Glu	Ile	Lys	Glu	Lys	Ile	Gly
1300						1305					1310				
Thr	Arg	Ser	Ala	Glu	Asp	Pro	Val	Ser	Glu	Val	Pro	Ala	Val	Ser	Gln
1315						1320					1325				
His	Pro	Arg	Thr	Lys	Ser	Ser	Arg	Leu	Gln	Gly	Ser	Ser	Leu	Ser	Ser
1330						1335					1340				

Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser		
1345	1350	1355
Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr		
1365	1370	1375
Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser		
1380	1385	1390
Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu		
1395	1400	1405
Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro		
1410	1415	1420
Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro		
1425	1430	1435
1440		
Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys		
1445	1450	1455
Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val		
1460	1465	1470
Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu		
1475	1480	1485
Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser		
1490	1495	1500
Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val		
1505	1510	1515
1520		
Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu		
1525	1530	1535
Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu		
1540	1545	1550
Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp		
1555	1560	1565
Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro		
1570	1575	1580
Thr Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys		
1585	1590	1595
1600		
Leu Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys		
1605	1610	1615
Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe		
1620	1625	1630

Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro  
1635 1640 1645

Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser  
1650 1655 1660

Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln  
1665 1670 1675 1680

Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser  
1685 1690 1695

Thr Asp Glu Ala Gln Gly Lys Thr Ser Ser Val Thr Ile Pro Glu  
1700 1705 1710

Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile  
1715 1720 1725

Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys  
1730 1735 1740

Lys Ile Met Asp Gln Val Gln Ala Ser Ala Ser Ser Ser Ala Pro  
1745 1750 1755 1760

Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val  
1765 1770 1775

Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn  
1780 1785 1790

Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn  
1795 1800 1805

Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn  
1810 1815 1820

Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe  
1825 1830 1835 1840

Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe  
1845 1850 1855

Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val  
1860 1865 1870

Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys  
1875 1880 1885

Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln  
1890 1895 1900

Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg  
1905 1910 1915 1920

Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser  
 1925 1930 1935  
Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln  
 1940 1945 1950  
Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser  
 1955 1960 1965  
Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn  
 1970 1975 1980  
Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser  
 1985 1990 1995 2000  
Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp  
 2005 2010 2015  
Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile  
 2020 2025 2030  
Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro  
 2035 2040 2045  
Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser  
 2050 2055 2060  
Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu  
 2065 2070 2075 2080  
Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser  
 2085 2090 2095  
Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val  
 2100 2105 2110  
Ser Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala  
 2115 2120 2125  
Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu  
 2130 2135 2140  
Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr  
 2145 2150 2155 2160  
Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu  
 2165 2170 2175  
Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys  
 2180 2185 2190  
Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu

2195	2200	2205
<u>Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile</u>		
2210	2215	2220
<u>Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser</u>		
2225	2230	2235
<u>Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro</u>		
2245	2250	2255
<u>Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg</u>		
2260	2265	2270
<u>Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln</u>		
2275	2280	2285
<u>Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser</u>		
2290	2295	2300
<u>Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro</u>		
2305	2310	2315
<u>2320</u>		
<u>Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile</u>		
2325	2330	2335
<u>Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser</u>		
2340	2345	2350
<u>Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser</u>		
2355	2360	2365
<u>Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu</u>		
2370	2375	2380
<u>Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly</u>		
2385	2390	2395
<u>2400</u>		
<u>Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu</u>		
2405	2410	2415
<u>Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser</u>		
2420	2425	2430
<u>Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro</u>		
2435	2440	2445
<u>Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser</u>		
2450	2455	2460
<u>Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln</u>		
2465	2470	2475
<u>2480</u>		

Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His  
 2485 2490 2495  


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Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser  
 2500 2505 2510  


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Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile  
 2515 2520 2525  


---

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser  
 2530 2535 2540  


---

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg  
 2545 2550 2555 2560  


---

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala  
 2565 2570 2575  


---

Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val  
 2580 2585 2590  


---

Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala  
 2595 2600 2605  


---

Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn  
 2610 2615 2620  


---

Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser  
 2625 2630 2635 2640  


---

Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp  
 2645 2650 2655  


---

Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly  
 2660 2665 2670  


---

Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu  
 2675 2680 2685  


---

Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln  
 2690 2695 2700  


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Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn  
 2705 2710 2715 2720  


---

Arg Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr  
 2725 2730 2735  


---

Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn  
 2740 2745 2750  


---

Glu Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser  
 2755 2760 2765

<u>Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe</u>
2770                    2775                    2780
<u>Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala</u>
2785                    2790                    2795                    2800
<u>Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg</u>
2805                    2810                    2815
<u>Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys</u>
2820                    2825                    2830
<u>Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val</u>
2835                    2840

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: ral2(yeast)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Gly Ala Lys Gly Leu Gln Leu Arg Ala Leu Arg Arg Ile Ala
1                        5                        10                        15

Arg Ile Glu Gln Gly Gly Thr Ala Ile Ser Pro Thr Ser Pro Leu
20                      25                        30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:

(B) CLONE: m3 (mAChR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys Arg Thr Lys Glu Leu  
1                   5                   10                   15

Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu Thr Glu  
20                   25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: MCC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu  
1                   5                   10                   15

Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu Thr Ala Met  
20                   25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATCAAGAC TGTGACTTTT AATTGTAGTT TATCCATT

40

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTAGAATT CATGTTAATA TATTGTGTC TTTTAACAG

40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTAGATTTA AAAAGGTGTT TTAAAATAAT TTTTAAGCT

40

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCAATTGT TGTATAAAAA CTTGTTCTA TTTTATTTAG

40

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTAACTTTC TTCATATAGT AAACATTGCC TTGTGTACTC

40

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

NNNNNNNNNN NNNGTCCCTT TTTTAAAAAA AAAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAAGTAACT TGGCAGTACA ACTTATTGAACTTTAATA

40

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACAAGATA TTGATACTTT TTTATTATTGTGGTTTAG

40

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTTACT TGTTTCTAAG TGATAAAACA GYGAAGAGCT

40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATAAAAACA TAACTAATTA GGTTTCTTGT TTTATTTAG

40

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTAGTAAAT TSCCTTTTT GTTTGTGGGT ATAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCATTTTG CATGTACTGA TGTAACTCC ATCTAACAG

40

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTAAATAAAT TATTATCA TATTTTAA AATTATTTAA

40

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATGATGTTA TCTGTATTTA CCTATAGTCT AAATTATACC ATCTATAATG TGCTTAATTT

60

TTAG

64

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTAACAGAAG ATTACAAACC CTGGTCACTA ATGCCATGAC TACTTGCTA AG

52

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGATATTAAA GTCGTAATT TGTTTCTAAA CTCATTGGC CCACAG

46

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTATGTTCTC TATAGTGTAC ATCGTAGTGC ATGTTCAAA

40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCATTGCT CTTCAAATAA CAAAGCATTA TGGTTTATGT TGATTTATT TTTCAG

56

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTAAGACAAA AATGTTTTT AATGACATAG ACAATTACTG GTG

43

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAGATGATT GTCTTTCC TCTTGCCCTT TTTAAATTAG

40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTT ATAACATGTA TTTCTTAAGA TAGCTCAGGT ATGA

44

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTGGCTTC AAGTTGNCTT TTTAATGATC CTCTATTCTG TATTTAATTT ACAG

54

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACTATTAA GAATTCACC TGTTTTCTT TTTCTCTTT TTCTTGAGG CAGGGTCTCA

60

CTCTG

65

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAACTAGTA TGATTATG TATAAATTAA TCTAAAATTG ATTAATTCC AG

52

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTACCTTGAA AACACATTAG TACTATAATA TGAATTCAT GT

42

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCAACTCNAATAGATGACC CATATTAGA AACTTACTAG

40

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATATAG AGTTTATAT TACTTTAAA GTACAGAATT CATACTCTCA AAAA

54

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATTGTGACCT TAATTTGTG ATCTCTTGAT TTTTATTCA G

41

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCCCGCCTG CCGCTCTC

18

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAGCGGC GG CTCCCGTG

18

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAACGGCT CTCATGCTGC

20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGTGCGGGG AGGAATGGA

19

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGATATCTT ACCAAATGAT ATAC

24

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATTCCTAC TTCTTCTATA CAG

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACCCATGCT GGCTCTTTT C

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGGGCCATC TTGTTCCCTGA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTAGGCA CAAAGCTTGC AA

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCAAGCTCC AGTAAGAAGG TA

22

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGCGGCTCCT GGGTTGTTG

19

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCCCTTCCT TTCTGAGGAC

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTTCTCCTG CCTCTTACTG C

21

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGACACCCC CCATTCCCTC

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCACTTAAAG CACATATATT TAGT

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTATGGAAAA TAGTGAAGAA CC

22

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCTTAAGTC CTGTTTTCT TTTG

24

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTTAGAACCT TTTTGTGTT GTG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCAGATTAT ACACTAAGCC TAAC

24

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CATGTCTCTT ACAGTAGTAC CA

22

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGGTCCAAGG GTAGCCAAGG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAAAAATGGA TAAACTACAA TTAAAAG

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAATACAGAA TCATGTCTTG AAGT

24

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACACCTAAAG ATGACAATT GAG

23

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAACTTAGAT AGCAGTAATT TCCC

24

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACAATAAACT GGAGTACACA AGG

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATAGGTCATT GCTTCTTGCT GAT

23

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGAATTTAA TGGATTACCT AGGT

24

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTTTTTTGCG TTTTACTGAT TAACG

25

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TGTAATTCAT TTTATTCCTA ATA[G]CCTC

27

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTAGCCATA GTATGATTAT TTCT

24

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTACCTATT TTATACCCAC AAAC

24

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAAAGCCT ACACCATTTC TGC

23

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCATTCTT AGAACCATCT TGC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCTATAGTC TAAATTATAAC CATC

24

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTCATGGCAT TAGTGACCAG

20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

AGTCGTAATT TTGTTCTAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGAAGGACTC GGATTCAC [G]C C

21

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCATTCACTC ACAGCCTGAT GAC

23

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCTTGAAAC ATGCACTACG AT

22

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AAACATCATT GCTCTCAAA TAAC

24

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TACCATGATT TAAAAATCCA CCAG

24

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATGATTGTC TTTTCCTCT TGC

23

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGAGCTATC TTAAGAAATA CATG

24

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTTTAAATGA TCCTCTATTC TGTAT

25

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACAGAGTCAG ACCCTGCCTC AAAG

24

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTCTATTCT TACTGCTAGC ATT

23

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATACACAGGT AAGAAATTAG GA

22

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TAGATGACCC ATATTCTGTT TC

22

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAATTAGGTC TTTTGAGAG TA

22

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTACTGCAT ACACATTGTG AC

22

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTTTGTT TCCTAACATG AAG

23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCCACAG GTAATACTCC C

21

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCTAGAACTG AATGGGTAC G

21

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAGGACAAAAA TAATCCTGTC CC

22

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTTTCTTAG TTTCATTCTT CCTC

24

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGAAGGATCC CTTGTGCAGT GTGGA

25

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

GACAGGATCC TGAAGCTGAG TTTG

24

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCAGAAAGTG CTGAAGAG

18

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGAATAATTAA GGTCTCCAA

19

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAATCCTA AGAGAGAACAA

21

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATGGCAAGCTTGAGCCAG

19

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTTCCAGCAG TGTCACAG

18

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGAGATTTC GCTCCTGA

18

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AGTACAAGGA TGCCAATATT ATG

23

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ACTTCTATCT TTTTCAGAAC GAG

23

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATTGAAATAC TACAGTGTAA CCC

23

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CTTGTATTCT AATTTGGCAT AAGG

24

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGCCCATAC ACATTCAAAC AC

22

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTTTGCGTC TTGCCCATCT T

21

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AGTCTTAAAT ATTCAAGATGA GCAG

24

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTTCTCTTC ATTATATTTT ATGCTA

26

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AAGCCTACCA ATTATAGTGA ACG

23

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AGCTGATGAC AAAGATGATA ATC

23

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAGAAACAAT ACAGACTTAT TGTG

24

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATGAGTGGGG TCTCCTGAAC

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATCTCCCTCC AAAAGTGGTG C

21

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TCCATCTGGA GTACTTCTG TG

22

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGTAAATGCT GCAGTCAGA GG

22

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCGTGGCATA TCATCCCC

19

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCCAGACTGC TTCAAAATTA CC

22

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAGCCTCATC TGTACTTCTG C

21

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CCCTCCAAAT GAGTTAGCTG C

21

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TTGTGGTATA GGTTTACTG GTG

23

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ACCCAACAAA AATCAGTTAG ATG

23

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GTGGCTGGTA ACTTTAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATGATGTTGA CCTTTCCAGG G

21

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATTGTGTAAC TTTCATCAG TTGC

24

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AAAGACATAC CAGACAGAGG G

21

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTTTTTGGC ATTGCAGGAGC T

21

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

AAGATGACCT GTTGCAGGAA TG

22

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATCAGACC AAGCTTGTCT AGAT

24

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CAATAGTAAG TAGTTACAT CAAG

24

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

AAACAGGACT TGTACTGTAG GA

22

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CAGCCCCTTC AAGCAACAT C

21

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAGGACTTAT TCCATTCTA CC

22

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CAGTCTCCTG GCCGAAACTC

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTTGACTGGC GTACTAATAC AG

22

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TGGTAATGGA GCCAATAAAA AGG

23

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

TGGGACTTTT CGCCATCCAC

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TGTCTCTATC CACACATTG TC

22

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ATGTTTTCA TCCTCACTTT TTGC

24

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGAGAAGAAC TGGAAGTTCA TC

22

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGAATCTTT AATGTTGGA TTTGC

25

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCTCCACAG GTAATACTCC C

21

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GCTACAAC TG AATGGGGTAC G

21

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CAGGACAAAA TAATCCTGTC CC

22

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ATTTTCTTAC TTTCATTCTT CCTC

24

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial sequence (consensus)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Phe Xaa Val Glu Xaa Thr Pro Xaa Cys Phe Ser Arg Xaa Ser Ser Leu Ser Ser Leu  
1 5 10 15

Ser  
20

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Tyr	Cys	Val	Glu	Asp	Thr	Pro	Ile	Cys	Phe	Ser	Arg	Cys	Ser	Ser	Leu
1															15
Ser	Ser	Leu	Ser												
															20

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

His	Thr	Val	Gln	Glu	Thr	Pro	Leu	Met	Phe	Ser	Arg	Cys	Thr	Ser	Val
1															15
Ser	Ser	Leu	Asp												
															20

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Phe	Ala	Thr	Glu	Ser	Thr	Pro	Asp	Gly	Phe	Ser	Cys	Ser	Ser	Ser	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1                   5                   10                   15  
Ser Ala Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr Ser Leu  
1                   5                   10                   15  
Ser Asp Leu Thr  
20

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu  
1                   5                   10                   15  
Ser Ser Leu Asp  
20

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Phe	Ala	Ile	Glu	Asn	Thr	Pro	Val	Cys	Pro	Ser	His	Asn	Ser	Ser	Leu
1					5				10					15	
Ser	Ser	Leu	Ser												
					20										

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Arg	His	Val	Glu	Asp	Thr	Pro	Val	Cys	Phe	Ser	Arg	Asn	Ser	Ser	Leu
1						5				10				15	
Ser	Ser	Leu	Ser												
					20										